

# SEQUENCE LISTING

<110> ANDERSON, DARRELL R.  
HANNA, NABIL  
BRAMS, PETER  
HEARD, CHERYL

<120> TREATMENT OF CROHN'S DISEASE USING ANTI-CD80 ANTIBODIES THAT  
DO NOT INHIBIT THE BINDING OF CD80 ANTIGEN TO CTLA-4

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<140> 09/576,424

<141> 2000-05-22

<150> PCT/US97/19906

<151> 1997-10-29

<150> 08/746,361

<151> 1996-11-08

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<170> PatentIn Ver. 2.1

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Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln	
20 25 30	
Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe	
35 40 45	
Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro	
50 55 60	
Glu Trp Val Gly Phe Ile Arg Asn Lys Pro Asn Gly Gly Thr Thr Glu	
65 70 75 80	
Tyr Ala Ala Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser	
85 90 95	
Lys Ser Ile Ala Tyr Leu Gln Met Ser Ser Leu Lys Ile Glu Asp Thr	
100 105 110	
Ala Val Tyr Tyr Cys Thr Thr Ser Tyr Ile Ser His Cys Arg Gly Gly	
115 120 125	
Val Cys Tyr Gly Gly Tyr Phe Glu Phe Trp Gly Gln Gly Ala Leu Val	
130 135 140	
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala	

145					150						155				160
Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu
				165					170					175	
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly
			180					185					190		
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser
		195					200					205			
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
	210					215					220				
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr
225					230					235					240
Lys	Val	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr
				245					250					255	
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
			260					265						270	
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
		275					280					285			
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
	290					295					300				
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
305					310						315				320
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
				325					330					335	
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
			340					345					350		
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
		355					360					365			
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
	370					375					380				
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
385					390					395					400
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
				405					410					415	
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
			420					425					430		
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
		435					440					445			
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
	450					455					460				
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
465					470					475					

<210> 9  
 <211> 711  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) .. (708)

<400> 9  
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 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro  
 1 5 10 15

ggt gca cga tgt gag tct gcc ctg aca cag ccg ccc tca gtg tct ggg 96  
 Gly Ala Arg Cys Glu Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Gly  
 20 25 30

gcc cca ggg cag aag gtc acc atc tcg tgc act ggg agc acc tcc aac 144  
 Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn  
 35 40 45

att gga ggt tat gat cta cat tgg tac cag cag ctc cca gga acg gcc 192  
 Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
 50 55 60

ccc aaa ctc ctc atc tat gac att aac aag cga ccc tca gga att tct 240  
 Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser  
 65 70 75 80

gac cga ttc tct ggc tcc aag tct ggt acc gcg gcc tcc ctg gcc atc 288  
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile  
 85 90 95

act ggg ctc cag act gag gat gag gct gat tat tac tgc cag tcc tat 336  
 Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr  
 100 105 110

gac agc agc ctg aat gct cag gta ttc gga gga ggg acc cgg ctg acc 384  
 Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr  
 115 120 125

gtc cta ggt cag ccc aag gct gcc ccc acg gtc act ctg ttc ccg ccc 432  
 Val Leu Gly Gln Pro Lys Ala Ala Pro Thr Val Thr Leu Phe Pro Pro  
 130 135 140

tcc tct gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata 480  
 Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile  
 145 150 155 160

agt gac ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc 528  
 Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser  
 165 170 175

agc ccc gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc 576  
 Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser  
 180 185 190

aac aac aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag 624

Asn	Asn	Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln		
		195					200					205					
tgg	aag	tcc	cac	aga	agc	tac	agc	tgc	cag	gtc	acg	cat	gaa	ggg	agc	672	
Trp	Lys	Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser		
	210					215					220						
acc	gtg	gag	aag	aca	gtg	gcc	cct	aca	gaa	tgt	tca	tga				711	
Thr	Val	Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser						
225					230					235							

<210> 10  
 <211> 236  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro  
 1 5 10 15  
 Gly Ala Arg Cys Glu Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Gly  
 20 25 30  
 Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn  
 35 40 45  
 Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
 50 55 60  
 Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser  
 65 70 75 80  
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile  
 85 90 95  
 Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr  
 100 105 110  
 Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr  
 115 120 125  
 Val Leu Gly Gln Pro Lys Ala Ala Pro Thr Val Thr Leu Phe Pro Pro  
 130 135 140  
 Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile  
 145 150 155 160  
 Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser  
 165 170 175  
 Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser  
 180 185 190  
 Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln  
 195 200 205  
 Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser  
 210 215 220

Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
 225 230 235

<210> 11  
 <211> 1431  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1428)

<400> 11  
 atg aaa cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg 48  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15  
 gtc ctg tcc cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag 96  
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
 20 25 30  
 cct tcg gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tcc atc 144  
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile  
 35 40 45  
 agc ggt ggt tat ggc tgg ggc tgg atc cgc cag ccc cca ggg aag ggg 192  
 Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly  
 50 55 60  
 ctg gag tgg att ggg agt ttc tat agt agt agt ggg aac acc tac tac 240  
 Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr  
 65 70 75 80  
 aac ccc tcc ctc aag agt caa gtc acc att tca aca gac acg tcc aag 288  
 Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys  
 85 90 95  
 aac cag ttc tcc ctg aag ctg aac tct atg acc gcc gcg gac acg gcc 336  
 Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala  
 100 105 110  
 gtg tat tac tgt gtg aga gat cgt ctt ttt tca gtt gtt gga atg gtt 384  
 Val Tyr Tyr Cys Val Arg Asp Arg Leu Phe Ser Val Val Gly Met Val  
 115 120 125  
 tac aac aac tgg ttc gat gtc tgg ggc ccg gga gtc ctg gtc acc gtc 432  
 Tyr Asn Asn Trp Phe Asp Val Trp Gly Pro Gly Val Leu Val Thr Val  
 130 135 140  
 tcc tca gct agc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc 480  
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
 145 150 155 160  
 tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag 528  
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Leu Gly Cys Leu Val Lys  
 165 170 175  
 gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg 576  
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
 180 185 190

acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc	624
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
195 200 205	
tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc	672
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
210 215 220	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg	720
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
225 230 235 240	
gac aag aaa gca gag ccc aaa tct tgt gac aaa act cac aca tgc cca	768
Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	
245 250 255	
ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc	816
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe	
260 265 270	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	864
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
275 280 285	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	912
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
290 295 300	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	960
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
305 310 315 320	
cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc	1008
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
325 330 335	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	1056
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
340 345 350	
tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc	1104
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	
355 360 365	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg	1152
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
370 375 380	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc	1200
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
385 390 395 400	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg	1248
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
405 410 415	
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gag ggc tcc	1296
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
420 425 430	



ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag	1344
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln	
435 440 445	
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac	1392
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His	
450 455 460	
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga	1431
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
465 470 475	

<210> 12  
 <211> 476  
 <212> PRT  
 <213> Homo sapiens

<400> 12	
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
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Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
20 25 30	
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile	
35 40 45	
Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly	
50 55 60	
Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr	
65 70 75 80	
Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys	
85 90 95	
Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala	
100 105 110	
Val Tyr Tyr Cys Val Arg Asp Arg Leu Phe Ser Val Val Gly Met Val	
115 120 125	
Tyr Asn Asn Trp Phe Asp Val Trp Gly Pro Gly Val Leu Val Thr Val	
130 135 140	
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser	
145 150 155 160	
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys	
165 170 175	
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
180 185 190	
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
195 200 205	
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
210 215 220	

Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	225	230	235	240
Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	245	250	255	
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	260	265	270	
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	275	280	285	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	290	295	300	
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	305	310	315	320
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	325	330	335	
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	340	345	350	
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	355	360	365	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	370	375	380	
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	385	390	395	400
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	405	410	415	
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	420	425	430	
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	435	440	445	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	450	455	460	
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					465	470	475	